

Figure 1A

1	CCACCGCGTCCGGGAGCTTGCACAACTACAATGGCTCTAAAAGCACAGATGAC	60
61	CTGCTACACTTCCTGACTTGCTTGTATTGGTGGCACTGTTCATAAATATAATTTGCTC	120
121	TTTCACTTTCTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA	180
181	GAGGCAGCAGAAGCCAGGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG	240
241	CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTGAC	300
301	TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCAATTGAT	360
361	AAGGGAAAATAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT	420
421	GTGAGCAACGTGGAAGATGGGTGATTCTGCATTTCAACTGAGCATGGAGAGAAAAATT	480
481	TATGTCCTTGCACCACATCCATCTCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA	540
1	M E P N G T F S N	9
541	TAACAACAGCAGGAACTGCACAATTGAAAACCTCAAGAGAGAATTTCCTCAATTGTATA	600
10	N N S R N C T I E N F K R E F F P I V Y	29
601	TCTGATAATATTTTCTGGGGAGTCTGGAAATGGGTGTCCATATATGTTTCCTGCA	660
30	<u>L I I F F W G V L G N G L S I Y V F L Q</u>	49
661	GCCTTATAAGAACATCTGTGAACGTTTCATGCTAAATCTGCCATTCAGATCT	720
50	P Y K K S T S V N V F M L N L A I S D L	69
721	CCTGTTCATAGCACGCTTCCCTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGAT	780
70	<u>L F I S T L P F R A D Y Y L R G S N W I</u>	89
781	ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCTTGTATGTCAACATGTACAGCAG	840
90	F G D L A C R I M S Y S L Y V N M Y S S	109
841	TATTTATTCCTGACCGTGTGAGTGTGCGTTCTGGCAATGGTCACCCCTTCG	900
110	<u>I Y F L T V L S V V R F L A M V H P F R</u>	129

**Figure 1B**

901 GCTTCTGCATGTCAACCAGCATCAGGAGTCCTGGATCTCTGTGGATCATATGGATCCT 960  
 130 L L H V T S I R S A W I L C G I I W I L 149  
 . . .  
 961 TATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTAC 1020  
 150 I M A S S I M L L D S G S E Q N G S V T 169  
 . . .  
 1021 ATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACATATATTGC 1080  
 170 S C L E L N L Y K I A K L Q T M N Y I A 189  
 . . .  
 1081 CTTGGTGGGGCTGCCTGCTGCCATTTCACACTCAGCATCTGTTATCTGCTGATCAT 1140  
 190 L V V G C L L P F F T L S I C Y L L I I 209  
 . . .  
 1141 TCGGGTTCTGTTAAAAGTGGAGGTCCCAGAACATGGGGCTGCGGGTTCTCACAGGAAGGC 1200  
 210 R V L L K V E V P E S G L R V S H R K A 229  
 . . .  
 1201 ACTGACCACCATCATCACCTGATCATCTTCTTGTTCTGCCCTATCACAC 1260  
 230 L T T I I I T L I I F F L C F L P Y H T 249  
 . . .  
 1261 ACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTATGCAAAGACAGACTGCATAA 1320  
 250 L R T V H L T T W K V G L C K D R L H K 269  
 . . .  
 1321 AGCTTTGGTTATCACACTGGCCTGGCAGCAGCCAATGCCGCTCAATCCTCTGCTCTA 1380  
 270 A L V I T L A L A A A N A C F N P L L Y 289  
 . . .  
 1381 TTACTTTGCTGGGAGAATTAAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCC 1440  
 290 Y F A G E N F K D R L K S A L R K G H P 309  
 . . .  
 1441 ACAGAAGGCAAAGACAAAGTGTGTTTCCCTGTTAGTGTGGTTGAGAAAGGAAACAAG 1500  
 310 Q K A K T K C V F P V S V W L R K E T R 329  
 . . .  
 1501 AGTATAAGGAGCTCTAGATGAGACCTGTTCTGTATCCTGTGTCATCTCATTCACT 1560  
 330 V \* 331  
 . . .  
 1561 CATAGTCTCAAATGACTTTGTATTTACATCACTCCAACAAATGTTGATTCTTAATATT 1620  
 . . .  
 1621 TAGTTGACCATTACTTTGTTAATAAGACCTACTTCAAAAATTATTCACTGTAAAAAA 1680  
 . . .  
 1681 AAAAAAAAAAAAAAAAAAAAAAA 1708

Figure 2A

1 50

HGPRBMY11	(1) -----MSLOPSISVSEMEPNC-----	-TFSNNSRNCIEN--FK
HGPRBMY11v1	(1) MERKFMSLQPSISVSEMEPNC-----	-TFSNNNSRNCIEN--FK
P2Y5_CHICK	(1) -----	-MVSSNQSTEDS-FK
P2YR_CHICK	(1) MTEALISAALNGTQPEELLAGG-----	-WAACNAATTKGSITKTGFO
P2YR_MELGA	(1) MTEALISAALNGTQPEELLAGG-----	-WAACNAATTKGSITKTGFO
P2YR_RAT	(1) MTEVPWSAVPNGTDAAFLAGLGSLGWNSTIASTAAVSSSFRCALIKTGFO-----	-NLTVSSATGHD TIDDFR
Q9Y271	(1) -----MDETG-----	-LTNFSLATAEQQGQETPEE
GPRH_HUMAN	(1) -----MNGLLEVAPP-----	

51 100

HGPRBMY11	(22) REFFPIVYIILIFEWGVVLGNGLSIYVFLQPYKKSTSVDVNFMENLAISDLIE-----	
HGPRBMY11v1	(38) REFFPIVYIILIFEWGVVLGNGLSIYVFLQPYKKSTSVDVNFMENLAISDLIE-----	
P2Y5_CHICK	(14) YTLIGCVESMVEVIGLITANCVAIYIFTITLKVRNETTTYMDLNLAISDLIE-----	
P2YR_CHICK	(40) FYYLPTVYILVFITGFLGNSVAIWMFVHFMRPWSGISVYMFNLALADELY-----	
P2YR_MELGA	(40) FYYLPTVYILVFITGFLGNSVAIWMFVHFMRPWSGISVYMFNLALADELY-----	
P2YR_RAT	(51) FYYLPAVYILVFITGFLGNSVAIWMFVHFHKPWSGISVYMFNLALADELY-----	
Q9Y271	(23) NQVYSTLISMISVWGFEGNGFVYVLIKTHKSAFOVYMINLAVALDLIC-----	
GPRH_HUMAN	(31) NMIFASFYLLDFILALVGNTIALWLFIRDHKSGTPANVBFEMHLAVADILSC-----	

101 150

HGPRBMY11	(72) I <del>STL</del> PF <del>RAD</del> YY <del>Y</del> ERGSN <del>W</del> IFGDI <del>A</del> CRIMSY <del>S</del> IYVNMY <del>S</del> IYFLIVLSVVR <del>F</del> -----	
HGPRBMY11v1	(88) I <del>STL</del> PF <del>RAD</del> YY <del>Y</del> ERGSN <del>W</del> IFGDI <del>A</del> CRIMSY <del>S</del> IYVNMY <del>S</del> IYFLIVLSVVR <del>F</del> -----	
P2Y5_CHICK	(64) VFTLPP <del>F</del> RIYYEVVRN-WPFGDVMCKLQR <del>F</del> IFHHVNLYGSILFLTCISVDR <del>F</del> -----	
P2YR_CHICK	(90) VLTLPA <del>L</del> I <del>F</del> YYFNKTDWIFGDVMCKLQR <del>F</del> IFHHVNLYGSILFLTCISVHR <del>F</del> -----	
P2YR_MELGA	(90) VLTLPA <del>L</del> I <del>F</del> YYFNKTDWIFGDVMCKLQR <del>F</del> IFHHVNLYGSILFLTCISVHR <del>F</del> -----	
P2YR_RAT	(101) VLTLPA <del>L</del> I <del>F</del> YYFNKTDWIFGDVMCKLQR <del>F</del> IFHHVNLYGSILFLTCISAH <del>F</del> -----	
Q9Y271	(73) VCTLPLRVYYVHKG <del>I</del> W <del>I</del> FGDFL <del>C</del> RLSTY <del>A</del> LYVNLYCS <del>I</del> FFMTAMSFFRC-----	
GPRH_HUMAN	(81) VLVLPLTR <del>E</del> VYH <del>F</del> SGNHWP <del>F</del> GET <del>A</del> CR <del>L</del> TGF <del>F</del> YL <del>N</del> MYAS <del>I</del> YFLTCISADRF-----	

151 200

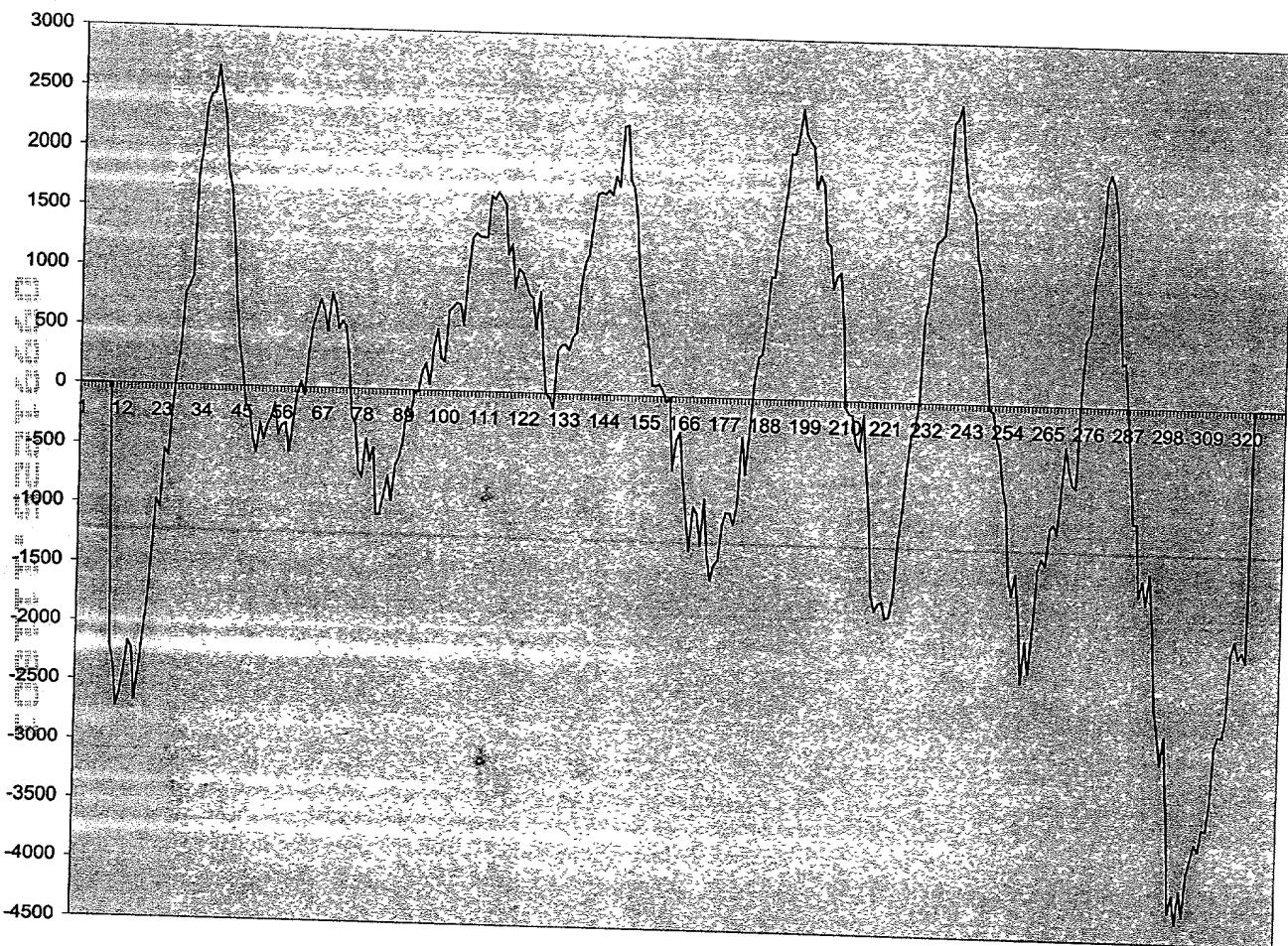
HGPRBMY11	(122) LAMVHP <del>F</del> RLIHVT <del>S</del> IRS <del>A</del> WILCG <del>I</del> WILIMASSIML <del>D</del> S-----GSEONGSV-----	
HGPRBMY11v1	(138) LAMVHP <del>F</del> RLIHVT <del>S</del> IRS <del>A</del> WILCG <del>I</del> WILIMASSIML <del>D</del> S-----GSEONGSV-----	
P2Y5_CHICK	(113) LAIVHP <del>F</del> RSK <del>T</del> IRTKRNARI <del>V</del> CVAVWITVLAGSTPA <del>S</del> EFQ <del>S</del> TNRQNTEQ-----	
P2YR_CHICK	(140) TGVVHPL <del>K</del> SLGR <del>L</del> KKKN <del>A</del> YV <del>S</del> SLV <del>W</del> ALVVAVIA <del>P</del> ILFY <del>S</del> CTGVRRNKT <del>I</del> -----	
P2YR_MELGA	(140) TGVVHPL <del>K</del> SLGR <del>L</del> KKKN <del>A</del> YV <del>S</del> SLV <del>W</del> ALVVAVIA <del>P</del> ILFY <del>S</del> CTGVRRNKT <del>I</del> -----	
P2YR_RAT	(151) SGVWYPL <del>K</del> SLGR <del>L</del> KKKN <del>A</del> YV <del>S</del> VL <del>W</del> LVVVA <del>I</del> S <del>P</del> ILFY <del>S</del> CTGVRRNKT <del>I</del> -----	
Q9Y271	(123) IAI <del>V</del> FPVONINIVTO <del>Q</del> KARF <del>V</del> CVGI <del>W</del> IFV <del>L</del> ISSPFLMAKPQ <del>K</del> DEKNNT <del>K</del> -----	
GPRH_HUMAN	(131) LAIVHPV <del>K</del> SLKLRR <del>P</del> LYAHLACAFL <del>W</del> WVAVAMAP <del>L</del> VSPOTVQT <del>N</del> HTV <del>V</del> -----	

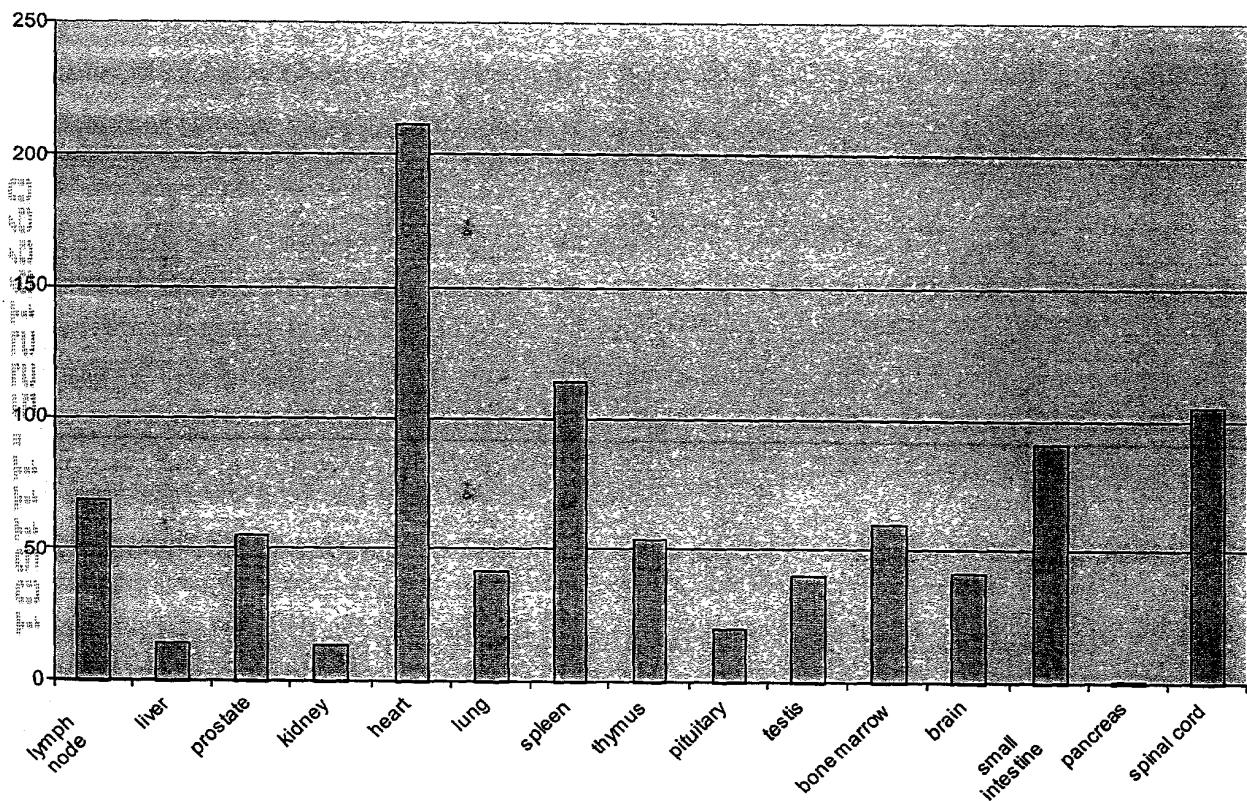
201 250

HGPRBMY11	(169) TSCLE--LNLYKIAKLOTMNYIALVVGC <del>L</del> LPFETES <del>I</del> CYLL <del>L</del> IRV <del>L</del> LKVE-----	
HGPRBMY11v1	(185) TSCLE--LNLYKIAKLOTMNYIALVVGC <del>L</del> LPFETES <del>I</del> CYLL <del>L</del> IRV <del>L</del> LKVE-----	
P2Y5_CHICK	(163) RTCFENFPESTWKTYLSRIV <del>I</del> FI <del>E</del> TVGH <del>F</del> IP <del>L</del> ILNVTC <del>S</del> TMV <del>I</del> RTLNKPL-----	
P2YR_CHICK	(190) TCYDT--TADEYLRSYFVYSMCTTVF <del>M</del> C <del>I</del> PF <del>V</del> ILG <del>C</del> YGLIVKAL <del>I</del> YKD-----	
P2YR_MELGA	(190) TCYDT--TADEYLRSYFVYSMCTTVF <del>M</del> C <del>I</del> PF <del>V</del> ILG <del>C</del> YGLIVKAL <del>I</del> YKD-----	
P2YR_RAT	(201) TCYDS--TSDEYLRSYF <del>I</del> YSMCTTVAMFC <del>I</del> PLV <del>V</del> ILG <del>C</del> YGLIVR <del>A</del> LYKD-----	
Q9Y271	(173) CFEPP--QDNQTKNHVLVLHYVSLFVGFI <del>I</del> PF <del>V</del> ILVCYTMI <del>I</del> L <del>L</del> LLKKS-----	
GPRH_HUMAN	(181) CLQLY-----REKASHHALVSLAVAF <del>T</del> FP <del>I</del> TTV <del>T</del> CYLL <del>L</del> IRSLRQGL-----	

**Figure 2B**

		251		
HGPRBMY11	(217)	VPESGLRVSHRKALTTIITLIIIFFLCFLPYHTLRTVHL		TWKV
HGPRBMY11v1	(233)	VPESGLRVSHRKALTTIITLIIIFFLCFLPYHTLRTVHL		TWKV
P2Y5_CHICK	(213)	TLSRNKLS-KKKVLEKMTIEVHLVIECFCEFPVNITLILYSLMR	--	TOTWIN
P2YR_CHICK	(238)	LDNSPLR--RKSTIYLVIIVLTVEAWSYLPFHVMKTLNLRARLDFQTPQM		
P2YR_MELGA	(238)	LDNSPLR--RKSTIYLVIIVLTVEAWSYLPFHVMKTLNLRARLDFQTPQM		
P2YR_RAT	(249)	LDNSPLR--RKSTIYLVIIVLTVEAWSYIIPFHVMKTMLNRARLDFQTPQM		
Q9Y271	(221)	MKKNLSS--HKKAIGMTMVVTAASFLVSFMPYHIQRTIHLHFLHN	--	ETKP
GPRH_HUMAN	(224)	RVEKRLK---TKAVRMIAIVIAIFIICFVFPYHVNRSSVYVLHYR	--	SHGAS
		301		
HGPRBMY11	(261)	GLCKDRLHKAIVITIALAAAANACENPLLYYFAGENFKDRLKSALRKGHPO		
HGPRBMY11v1	(277)	GLCKDRLHKAIVITIALAAAANACENPLLYYFAGENFKDRLKSALRKGHPO		
P2Y5_CHICK	(260)	GSVVTAVRTMYPVTLICIAVSNCFCDPIVYYFTSDINSELDK--KQQ--VH		
P2YR_CHICK	(285)	CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSRR		
P2YR_MELGA	(285)	CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSRR		
P2YR_RAT	(296)	CDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKASRR		
Q9Y271	(267)	CDSVIRMQSKSVITLSLAASNCFCDFLLYFFSGGNFRKRRLS-TERKHSL		
GPRH_HUMAN	(269)	CATORILALANRITSCLTSINGALDPIMYFFVAEKFRLHALCNLLCGKRLK		
		351	379	
HGPRBMY11	(311)	KAK-TKCVFPVSVWLRKETRV-----		
HGPRBMY11v1	(327)	KAK-TKCVFPVSVWLRKETRV-----		
P2Y5_CHICK	(306)	QNT-----		
P2YR_CHICK	(335)	SEP-NVQSKSEEMILNILTEYKONGDTSL		
P2YR_MELGA	(335)	SEP-NVQSKSEEMILNILTEYKONGDTSL		
P2YR_RAT	(346)	SEA-NLQSKSEEMILNILSEFKONGDTSL		
Q9Y271	(316)	SVT-YVPRKKASLPEKGEEICKV-----		
GPRH_HUMAN	(319)	GPPPSFEKGKTNSSLAKSEL-----		

**Figure 3**

**Figure 4.****Expression Profiling of Novel Human GPCR, HGPRBMY11**

**Figure 5.****HGPRBMY11**

<b>Protein</b>	<b>Genbank ID</b>	<b>Identities</b>	<b>Similarities</b>
human cysteinyl leukotriene receptor	gi 11422069	37%	49%
chick purinergic receptor 5	gi P32250	36%	46%
human G-protein-coupled receptor GPR17	gi Q13304	36%	46%
chick purinergic receptor	gi P34996	30%	45%
turkey purinergic receptor	gi P49652	30%	45%
rat purinergic receptor	gi P49651	30%	44%

**HGPRBMY11v1**

<b>Protein</b>	<b>Genbank ID</b>	<b>Identities</b>	<b>Similarities</b>
human cysteinyl leukotriene receptor	gi 11422069	37.2%	49%
chick purinergic receptor 5	gi P32250	36.7%	46.1%
human G-protein-coupled receptor GPR17	gi Q13304	36.2%	46.1%
chick purinergic receptor	gi P34996	29.5%	43.9%
turkey purinergic receptor	gi P49652	29.8%	44.2%
rat purinergic receptor	gi P49651	29.6%	44%

Figure 6A

1 ATGGAGAGAAAATTATGTCCTTGCACCATCCATCTCCGTATCAGAAATGGAACCAAAT 60  
 1 M E R K F M S L Q P S I S V S E M E P N 20

61 GGCACCTTCAGCAATAACAACAGCAGGAACACTGCACAAATTGAAAACCTCAAGAGAGAATT 120  
 21 G T F S N N N S R N C T I E N F K R E F 40

121 TTCCCAATTGTATATCTGATAATATTTCTGGGGAGTCTTGGAAATGGGTTGTCCATA 180  
 41 F P I V Y L I I F F W G V L G N G L S I 60

181 TATGTTTCCTGCAGCCTTATAAGAACGTCACATCTGTGAACGTTTCATGCTAAATCTG 240  
 61 Y V F L Q P Y K K S T S V N V F M L N L 80

241 GCCAATTTCAGATCTCCTGTTCATAGCACCGCTTCCCTTCAGGGCTGACTATTATCTAGA 300  
 81 A I S D L L F I S T L P F R A D Y Y L R 100

301 GGCTCCAATTGGATAATTGGAGACCTGGCCTGCAGGATTATGCTTATTCTGTATGTC 360  
 101 G S N W I F G D L A C R I M S Y S L Y V 120

361 AACATGTACAGCAGTATTATTCCTGACCGTGCTGAGTGTGCGTTCTGGCAATG 420  
 121 N M Y S S I Y F L T V L S V V R F L A M 140

421 GTTCACCCCTTCGGCTCTGCATGTACAGCATCAGGAGTGGCTGGATCCTCTGGGG 480  
 141 V H P F R L L H V T S I R S A W I L C G 160

481 ATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG 540  
 161 I I W I L I M A S S I M L L D S G S E Q 180

541 AACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC 600  
 181 N G S V T S C L E L N L Y K I A K L O T 200

601 ATGAACATATTGCCTTGGTGGTGGCTGCCATTTTACACTCAGCATCTGT 660  
 201 M N Y I A L V V G C L L P F F T L S I C 220

661 TATCTGCTGATCATTGGGTTCTGTTAAAGTGGAGGTCCCAGAACATGGGCTGGGGTT 720  
 221 Y L L I I R V L L K V E V P E S G L R V 240

721 TCTCACAGGAAGGCACTGACCAACCACATCACCATCACCTGATCATCTTCTTGTGTTTC 780  
 241 S H R K A L T T I I I T L I I F F L C F 260

781 CTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTATGCAA 840  
 261 L P Y H T L R T V H L T T W K V G L C K 280

841 GACAGACTGCATAAAGCTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCCTGCTTC 900  
 281 D R L H K A L V I T L A A A N A C F 300

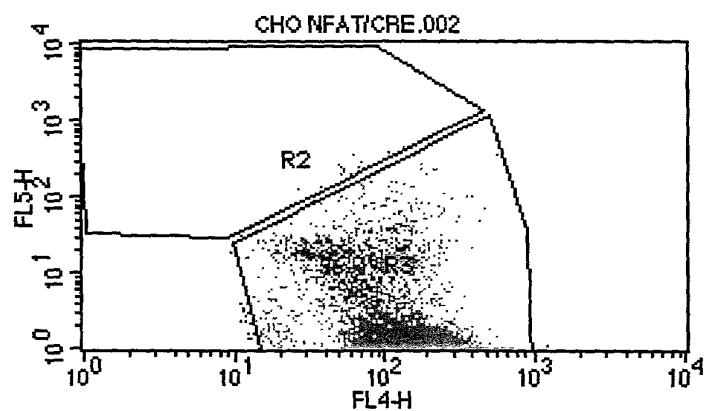
Figure 6B

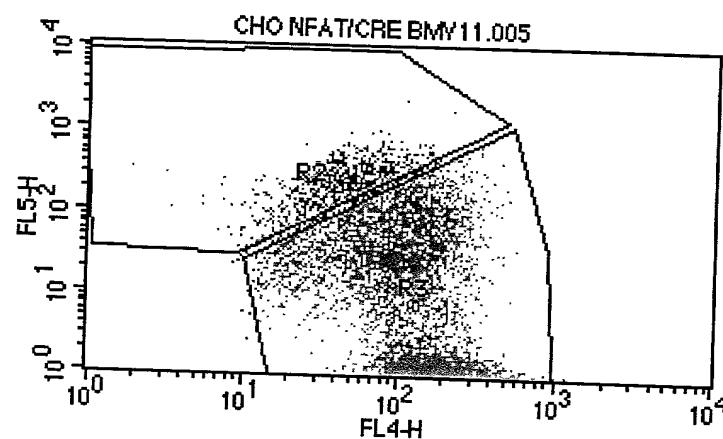
901 AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTAAAGGACAGACTAAAGTCTGCACTC 960  
301 N P L L Y Y F A G E N F K D R L K S A L 320

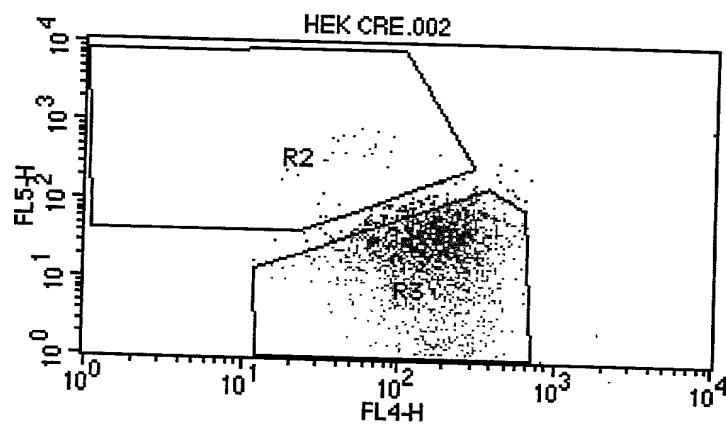
961 AGAAAAGGCCATCCACAGAACAGCAAAGACAAGTGTGTTCCCTGTTAGTGTGTGGTTG 1020  
321 R K G H P Q K A K T K C V F P V S V W L 340

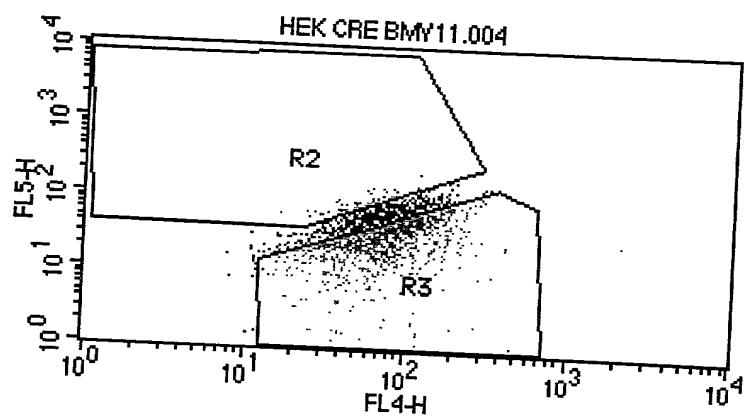
1021 AGAAAAGGAAACAAGAGTATAA 1041  
341 R K E T R V 346

Figure 7



**Figure 8**

**Figure 9**

**Figure 10**

**Figure 11**

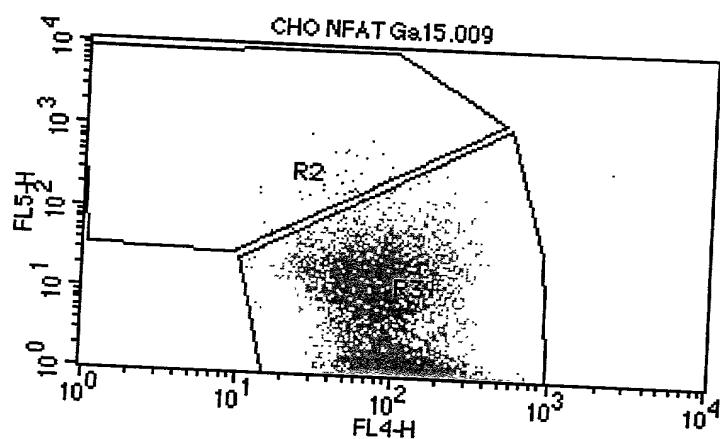


Figure 12

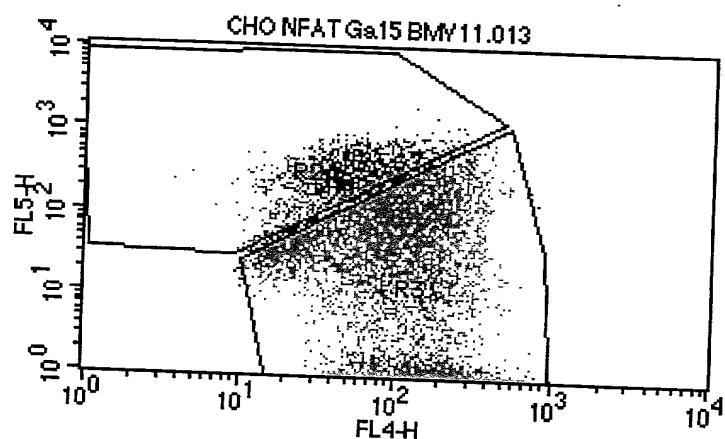
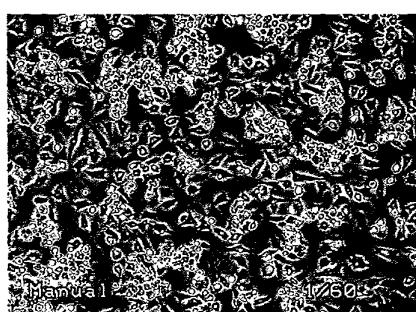
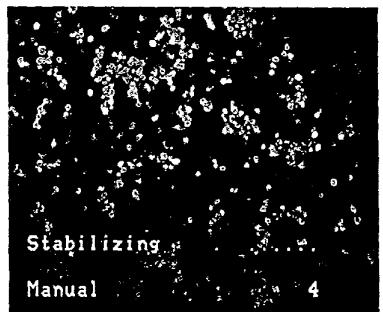


Figure 13

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)

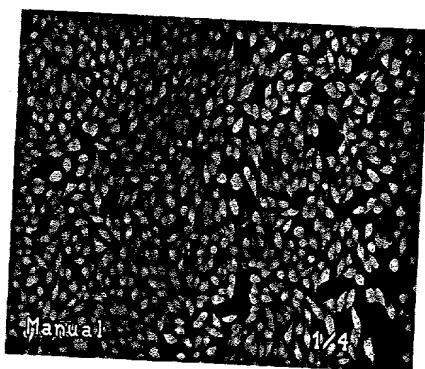


Cho NFAT Ga15 BMY11 (Fluorescent vs. Bright Field)

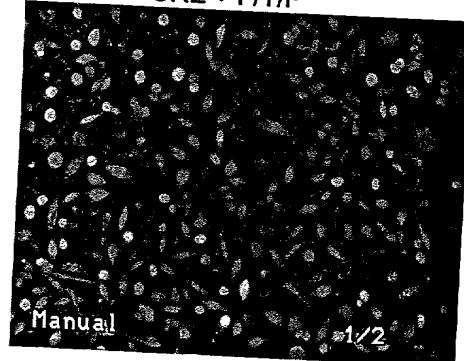


**Figure 14**

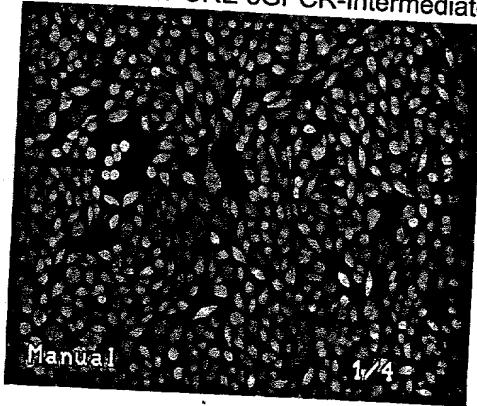
a. Cho-NFAT CRE



b. Cho-NFAT CRE + F/T/P



c. Cho-NFAT CRE oGPCR-Intermediate



d. Cho-NFAT CRE oGPCR High



Figure 15A

1	ATGTCCTTGCAACCACCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT	60
1	M S L Q P S I S V S E M E P N G T F S N	20
61	AACAACAGCAGGAAC TG CACAATTGAAAAC TT CAAGAGAGAATT T T T C C A A T T G T A T A T	120
21	N N S R N C T I E N F K R E F F P I V Y	40
121	CTGATAATATTTCTGGGAGTCTGGAAATGGGTGTCCATATATGTTTCTGCAG	180
41	L I I F F W G V L G N G L S I Y V F L Q	60
181	CCTTATAAGAACATCTGTGAACGTTTCATGCTAAATCTGCCATTCAAGATCTC	240
61	P Y K K S T S V N V F M L N L A I S D L	80
241	CTGTTCATAGCACCGCTCCCTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA	300
81	L F I S T L P F R A D Y Y L R G S N W I	100
301	TTTGGAGACCTGGCTGCAGGATTATGTCTTATTCTGTATGTCACATGTACAGCAGT	360
101	F G D L A C R I M S Y S L Y V N M Y S S	120
361	ATTTATTTCCTGACCGTGCTGAGTGTGCGTTCTGGCAATGGTCACCCCTTCGG	420
121	I Y F L T V L S V V R F L A M V H P F R	140
421	CTTCTGCATGTCAACCAGCATCAGGAGTGCCTGGATCCTCTGTGGATCATATGGATCCTT	480
141	L L H V T S I R S A W I L C G I I W I L	160
481	ATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCA	540
161	I M A S S I M L L D S G S E Q N G S V T	180
541	TCATGCTTAGAGCTGAATCTCTATAAAATGCTAAGCTGCAGACCATGAACTATATTGCC	600
181	S C L E L N L Y K I A K L Q T M N Y I A	200
601	TTGGTGGTGGCTGCCTGCTGCCATTTCACACTCAGCATCTGTTATCTGCTGATCATT	660
201	L V V G C L L P F F T L S I C Y L L I I	220
661	CGGGTTCTGTTAAAGTGGAGGTCCCAGAATCGGGCTGCAGGGTTCTCACAGGAAGGCA	720
221	R V L L K V E V P E S G L R V S H R K A	240
721	CTGACCACCATCATCACCTTGATCATCTCTTCTGTGTTCTGCCCTATCACACA	780
241	L T T I I T L I I F F L C F L P Y H T	260
781	CTGAGGACCGTCCACTTGACGACATGGAAAGTGGTTATGCAAAGACAGACTGCATAAA	840
261	L R T V H L T T W K V G L C K D R L H K	280
841	GCTTTGGTTATCACACTGGCCTGGCAGCAGCCAATGCCTGCTCAATCCTCTGCTCTAT	900
281	A L V I T L A L A A A N A C F N P L L Y	300

**Figure 15B**

901	TAC	TTG	C	GGG	GAGA	AT	TTA	A	GGC	A	CA	GACT	AA	AGT	CTG	CA	T	CAG	AAA	AGGCC	ATCCA		
301	Y	F	A	G	E	N	F	K	D	R	L	K	S	A	L	R	K	G	H	P			
961	CAGA	AGG	CAA	AG	ACA	AA	AGT	GT	TTT	CC	CTG	TT	AGT	GT	GT	GG	TT	GAG	AA	AGG	AA	ACA	AGA
321	Q	K	A	K	T	K	C	V	F	P	V	S	V	W	L	R	K	E	T	R			
1021	GTATAA																						
341	V																						

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